We claim:

1. A nucleic acid with a 5' end and a 3' end comprising a first functional nucleotide sequence and a scissile strand topoisomerase I cleavage motif sequence, wherein the scissile strand topoisomerase I cleavage motif sequence is located 3' to the first functional nucleotide sequence and provides a scissile strand topoisomerase I cleavage site that is not more than 10 bases from the 3' end of the nucleic acid.

2. The nucleic acid of claim 1, wherein the scissile strand topoisomerase cleavage motif sequence is selected from the group consisting of: CCCTT and TCCTT.

3. The nucleic acid of claim 1, wherein the first functional nucleotide sequence is selected from the group consisting of: a prokaryotic promoter sequence, a eukaryotic promoter sequence, a viral promoter sequence, a mutational sequence, a polypeptide tag encoding sequence, a nucleic acid tag sequence, a terminator sequence, a fusible protein encoding sequence, a radioactively labeled nucleotide sequence, a chemically labeled nucleotide sequence and an intronic sequence.

4. An adaptor comprising a first nucleic acid with a 5' end and a 3' end and comprising a scissile strand topoisomerase I cleavage motif having a 5' motif sequence contiguous with a 3' motif terminal nucleotide, said 3' motif terminal nucleotide being contiguous with a palindromic sequence of not less than two nucleotides nor more than 10 nucleotides and said palindromic sequence being contiguous with a 3' end nucleotide that is complementary to the 3' motif terminal nucleotide of the scissile strand topoisomerase I cleavage motif.

5. The adaptor of claim 4 further comprising a second nucleic acid having a 5' end sequence that is complementary to the 5' motif sequence of the scissile strand topoisomerase I cleavage motif.

6. The first nucleic acid of the adaptor of claim 4, wherein the 3' motif terminal nucleotide of the scissile strand topoisomerase I cleavage motif is T and the 5' motif sequence of the scissile strand topoisomerase I cleavage motif is selected from the group consisting of CCCT and TCCT.

7. The first nucleic acid of the adaptor of claim 4 further comprising a restriction endonuclease site located 5' to the scissile strand topoisomerase I cleavage motif.

8. The first nucleic acid of the adaptor of claim 4 further comprising a 5' end sequence that is complementary to the 5'-overhang of a restriction endonuclease site.

9. The first nucleic acid of claim 7 or claim 8, wherein the restriction endonuclease is selected from the group consisting of: BamH I, Bgl II, Cla I, Dde I, Eae I, Eag I, EcoR I, Hind III, Kas I,

Mbo I, Mlu I, Nco I, Nde I, Nhe I, Not I, PaeR7 I, Sal I, Sau3A, Spe I, Sty I, Xba I, Xho I and Xma I.

10. The first nucleic acid of the adaptor of claim 4, further comprising a first functional nucleotide sequence selected from the group consisting of: a prokaryotic promoter sequence, a eukaryotic promoter sequence, a viral promoter sequence, a mutational sequence, a polypeptide tag encoding sequence, a nucleic acid tag sequence, a terminator sequence, a fusible protein encoding sequence, a radioactively labeled nucleotide sequence, a chemically labeled nucleotide sequence and an intronic sequence.

11. A method for joining an adaptor sequence to a target nucleic acid sequence comprising:
providing a nucleic acid adaptor of claim 5,
providing a target nucleic acid with a one base 3' overhang nucleotide that is complementary to the 3' motif terminal nucleotide of the scissile strand topoisomerase cleavage motif, and
incubating the nucleic acid adaptor with the target nucleic acid in the presence of a topoisomerase I activity,
thereby joining the adaptor sequence to the target nucleic acid sequence.

12. The method of claim 11, wherein the first nucleic acid of the adaptor of claim 5 further comprises a functional nucleotide sequence that is 5' to the scissile strand topoisomerase I cleavage motif.

13. The method of claim 12, wherein the functional nucleotide sequence is selected from the group consisting of: a prokaryotic promoter sequence, a eukaryotic promoter sequence, a viral promoter sequence, a mutational sequence, a polypeptide tag encoding sequence, a nucleic acid tag sequence, a terminator sequence, a fusible protein encoding sequence, a radioactively labeled nucleotide sequence, an intronic sequence.

14. The method of claim 12, wherein the functional nucleotide sequence is a phage promoter selected from the group consisting of: an SP6 promoter, a T3 promoter and a T7 promoter.

15. The method of claim 11, further comprising the step of amplifying the joined product.

16. The method of claim 15, wherein the joined product is amplified by a polymerase chain reaction utilizing a first primer specific to the nucleic acid adaptor and a second primer specific to the target nucleic acid sequence.

17. The method of claim 11, wherein the target nucleic acid is generated by a polymerase chain reaction of a target genomic or a target cDNA sequence with a 5' sense strand primer and a 3' anti-sense strand primer.

18. The method of claim 17, wherein the adaptor provides a functional nucleotide sequence that is a promoter sequence and further comprising the steps of preparing at least two separate amplification reactions from the joined product comprising:

a first amplification reaction with 3' anti-sense strand primer and a first adaptor primer; and

a second amplification reaction with a 5' sense strand primer and a second adaptor primer, wherein the first adaptor primer comprises a sequence in the first nucleic acid of the adaptor and the second adaptor primer comprises a sequence in the second nucleic acid of the adaptor.

19. The method of claim 18 further comprising the step of isolating the product of either the first amplification reaction or the second amplification reaction.

20. The method of claim 19 further comprising contacting the amplification product with an RNA polymerase activity which recognizes said promoter sequence.